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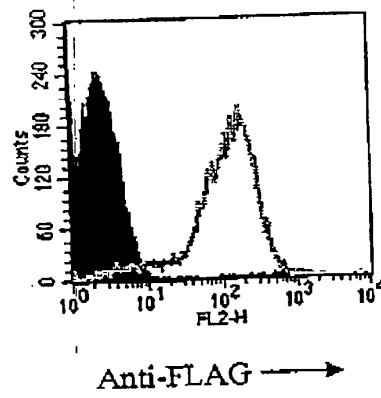


Figure 1

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10	30	50	70	90
1	110	130	150	170
ACCAC	TGCTTCATTGCTG	TGAGAAATGTTCC	AGGCTGAGTGA	GAAGTAATAAAATTCATCTCTGAGAACTCTTACCGGCTGTGGA
19	190	210	230	250
AGAAAT	CCAGAAATGTTGAT	TGGAGCAACTAGAGATATGG	AGAGGCGGCTTCTGCATGCGCTGAGTCTCTG	ATGCTGCTTATCTG
19	290	310	330	350
GTCAAT	TATACAAATGATGAATATTCAGTCTCTG	TGCCCCAGTGCATGAATGAATGCGGAGCTGCTTC	ACAGCGCCACACTGTGTTGTA	
49	370	390	410	430
E	GFWTGSENRRIIEPH	EKKCQDIN	ECLLEL	ELE
79	470	490	510	530
V	CKDVSYCRNKIKIGTYIC	SCVVKYPLFN	WVA	
109	550	570	590	610
G	INIDHPDCYV	NKSKNTGSKTH	TLGLSE	E
139	650	670	690	710
F	KSKEEVA	KGATKLLRLRKVE	HILNEN	SDIP
169	730	750	770	790
K	XDENPLLD	IVYE	TKRC	KTMTEAGNNTM
199	830	850	870	890
K	VDCTSGFK	EHNSGGET	ATAVA	FIAFKSLGNL
229	930	950	970	990
L	NGSFFSN	E	G	FQEZVT
259	1030	1050	1070	1090
L	NGSFFSN	E	G	FQEZVT

Figure 2

100709502 100709501
107070982

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910 930 950 970 990
259 K P V L S E P V L L T L Q N I Q P I D S R A E H L C V H W E 288
CAAACCTGCTCTCTGACCTGACTTACAAATATTCAGCCCATGACTCAAGACGAGACATCTCTGTGTCCATTGGGA 1070
1010
289 G S E G G S W S T K G C S H V Y T N N S Y T I C K C F H L 318
AGGATCAGAGGAGGGGAGCTGCTACCAAGAGTCTCTCAGGTGTACACCAATANTCTACACCATTTGCAAGTGTTCACCT 1170
1110
319 S S F A V L M A L P H E E D G V L S A L S V I T Y V G L S L 348
GTCCAGCTTTGCTGCTCATGGCTCTACCCCATGAGGAGGTGGTGTCTTCTGCTCTCTGTGATCACCTATGTGGGACTGAGTCT 1250
1190
349 S L C L F L A A I T F L L C R P I Q N T S T T L H L Q L S 378
TTCTCTGTGGCTATTTCTGGGGCCATCACTTTCTCTGCTGGGACCATTCAGATATCCAGACAGACATCCACCTGCAGCTCTC 1350
1270
379 I C L F L A D L F L T G I N R T K P K V L C S I I A G M L 409
CATCTGCCCTTTCTGGCTGACCTCTCTCCCTCAGAGCATCAACAGACTAAGCTAAGGTGCTGTGCTCCATCAATAGCGGGATGTT 1430
1370
409 H Y L Y L A S F M W M F L E G L H L F L T V S N L K V A N Y 438
GCACTACCTCTACTTGGCTTCTCTCATGGGATGTTCTCGAGGGCTACATCTTTTCTCAGTGTAGCAATCTCAAGTGGCCACTTA 1530
1450
439 S N S G R F K K R F M Y P V G Y G L P A F I V A V S A I A G 468
CAGCAACTCAGGCAGATTCAGAGAGGCTTCATGTATCTGTAGGATATGGGCTTCTGCTTTTATTTGTTGTTATCTGCAATAGCTGG 1610
1550
469 H K N Y G T H N H C W L S L H R G F I W S F L G P A A I I 498
CCACAGAAATATGGACACACACACCACTGCTGGCTCAGCCCTTCATGAGGATTCATCTGGAGCTTCTTGGGGCCAGCGGAGCCATTAT 1710
1630
499 L I N L V F Y F L I I W I L R S K L S S L N K E V S T L Q D 528
CTTGATTAACCTGGTGTCTACTTCTAATATATGGATTTTGGAGAGCAAACTTTCTTCTCATTAAGAGCTTTCTACACTTCAGA 1790
1730
529 T K V M T F K A I V O L F V L G C S W G I G L F I F I E V G 558
CACAAAGCTTATGACATTTAAAGCCATGCTCCAGTATTTGCTTGGGATGTTCTTGGGCAATGGCTTGTATTTTCTATTGAGTTGG

Figure 2 (continued)

1810 1830 1850 1870 1890
559 K T V R L I V A Y L F T I I N V L Q G V L I F M V H C L L N 588
GAACAGTGAGACTGATCGTTGGCTATCTGTTCCATCATCAATGTCCTGGAGGTGTTTCATATTTTNGGTACATTTGCTGCTTAA 1970
1910
589 R Q V R M E Y K K W F H R L R K E V E S E S T E V S H S T T 618
TCGCCAGGTGCGGATGAATATAAGAAGTGGTTCTAGACTCGCGAAGGAGTTCGAAGTGAAGACACTGAAGTGTCTCATTTCTACTAC 2070
2010
619 H T K M G L S L N L E N F C P T G N L H D P S D S I L P S T 648
TCACACAAATGGGTCTTTCTCTGAACCTGGAAATTTCTGCCCCACGAGGAACCTCCATGCTCTTCTGACTCCATCTCTCCAACTAC 2150
2090
649 E V A G V Y L S T P R S H M G A E D V N S G T H A Y W S R T 678
TGAAGTAGCAGGTGTATCTTAAGCACACCCCGGTCTCACATGGGTGCTGAGGATGTGAAGTACTCAGGTACTCAGCTTACTGGAGCAGAAC 2250
2170 2190
679 I S D 2270 2290 2310 2330
TATTAGTGATTGAATCAGCTCCTTCCCCCAAGCCTCTTACAGTACATTTTAACTGTGCTGCCATGCACATGAAGCTATATTGCTAG 2430
TCTGTPAAAACAACTGTTGCATATTCATGTCATTTTATCTCTACTTGCAAAAGTTAGCTTCTTTTATATCATTTTATTTTC 2410
2350 2370 2390 2410 2430
TCTTTCTTTTGTATATATAGCTTCAGTTGAGTGGGTTCTAGTCTTAAATGTTCTAGATCACTATTTTCTTTTCAGTTAACCTTTATTG 2510
2450 2470 2490 2510
GTATTTACTTCTCTGTGTAGTGTATACCACTGGNATATTTTATTTCTTAAATTTTGGGTTAAATATAGTTACATCATTTTCTCTTTT 2590 2610
2530 2550 2570 2590
TTCTTTCCACATCCTCCTGTATACCTTTTCCCTGGTGTCTATTTTATTTGTTTCTACATGCATATATATTTTATGCAAAACATATATAT 2690
2630 2650 2670 2690
GTATTAATATAATATATATTTCTTATATGATGAAACCACTACTCTCATCAATATATGTTCTTCTATGTATGTTTTCAGGACGCGGA 2790
2710 2730 2750 2770
CAACATAGCTATGGTAGCATGGCAGGGGAAAGCCACAGGACCTCAGCCCTATACAAAGAAATCAGAGGCACTGAGGAGTGTGAGTTG 2870
2810 2830 2850
AAGGAATTTGCTTACCCAGGGGACATTTATTTGGTTATCTAATACAAATGTTTCAGCCCCCAAACTGTTAAGATAAAGCCTATAT

Figure 2 (continued)

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2890 2910 2930 2950 2970
GCATCTAGGAAGTACTACCTTGATACACCTTATTGGATATCATCCACATGTTTATTCTGTGTTCTCGAAGAGGGTCTGTTGAATTTC
3050
GCATCTAGGAAGTACTACCTTGATACACCTTATTGGATATCATCCACATGTTTATTCTGTGTTCTCGAAGAGGGTCTGTTGAATTTC
2990 3010 3030 3050
TAAGGGTTGATCAGTTTAATTCGTGCCATTTTATATTCAGGGGTGTTGGCTTTGTTGTAGTGAATAATGCTATATTTCCCTGTTATCTGCA
3070 3090 3110 3130
TCTTTGACTCTTATTTTTCCTGGCGATACCTTATTTCACAAGAAGCTAGAGCGTTGGTTTATTACITTTTCTCCATAGAAAACTATT
3170 3190 3210 3230
TGCTTCCAGGATTAGATATGATCAATATTTCTATATGCAATGATCAATATCATGATGAATATATTAAGTGTATATTAATTAATGCTG
3250
GCAATTAAGTCCGAAGGA

Figure 2 (continued)

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[illegible]

Figure 3

Em1_Human Em1_Mouse Em1_Fla	401 AVVSECAQDM GVASFCLVNM TWTFPEGVHS	NITSVLDVVC ATFTLEHNTC QTLSPFPDKV	EMCTVVSLE CMKAPVSLU NKSCHTGSLE	NIQRSTVPEVL SAASTVRLVL THLGLVLSSE	450 KUISMWEKFI LDATITWII KLVDELMEZA
Cd97_Human	451 KEITYSSIAIV KEETSTLGLVI KEEVAKGAK	FCUSVUSMIL LLEIVETAIL LLAKVHNHIL	ASFWLPSAN AALLTPSGH NBSMDIKKD	VLPAAVRAIYL ASQMDOTIYL EHLGLDVIYLG	500 UI...ISAVI DE...GSLVI TK...ACSTAI
Cd97_Human	501 MKESRRHYVT MKECRRHES TK...	LNLVAKGDKM LNLAAGGDKM LNLAAGGDKM	RQVLSYIDV NVGCLPIIKH KVGCTSDPRED	SRLTETDQVA SVSTDAFQVA HNSHLETAVA	550 VVSFVDMER VVSFAHMS VIAVNSLHM
Em1_Human Em1_Mouse Em1_Fla	551 VLMERFTH VLNERFHE LLMUTFS	...DIQAP ...DQO ...NUR	LYTSRILXSN ...SRKRLRL ...OTDEVT	SRVYHUI SKVVGGL ...SVVSGA	600 NTOHKAIDNFS VTGRLVQVLS JASLVKPVLS
Cd97_Human	601 VLIITLTHV VLIITLTHV VLIITLTHV	QPKO QPKO QPKO	...K ...K ...S	FURPICVSW SERPICVSW SERPICVSW	650 TUVK...HUI TDVLE...HUI SGSE...HUI
Em1_Human Em1_Mouse Em1_Fla	651 VLIITLTHV VLIITLTHV VLIITLTHV	QPKO QPKO QPKO	...K ...K ...S	FURPICVSW SERPICVSW SERPICVSW	700 TUVK...HUI TDVLE...HUI SGSE...HUI
Cd97_Human	701 VLIITLTHV VLIITLTHV VLIITLTHV	QPKO QPKO QPKO	...K ...K ...S	FURPICVSW SERPICVSW SERPICVSW	750 TUVK...HUI TDVLE...HUI SGSE...HUI
Em1_Human Em1_Mouse Em1_Fla	751 VLIITLTHV VLIITLTHV VLIITLTHV	QPKO QPKO QPKO	...K ...K ...S	FURPICVSW SERPICVSW SERPICVSW	800 TUVK...HUI TDVLE...HUI SGSE...HUI
Cd97_Human	801 VLIITLTHV VLIITLTHV VLIITLTHV	QPKO QPKO QPKO	...K ...K ...S	FURPICVSW SERPICVSW SERPICVSW	850 TUVK...HUI TDVLE...HUI SGSE...HUI

Figure 3 (continued)

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Figure 3 (continued)

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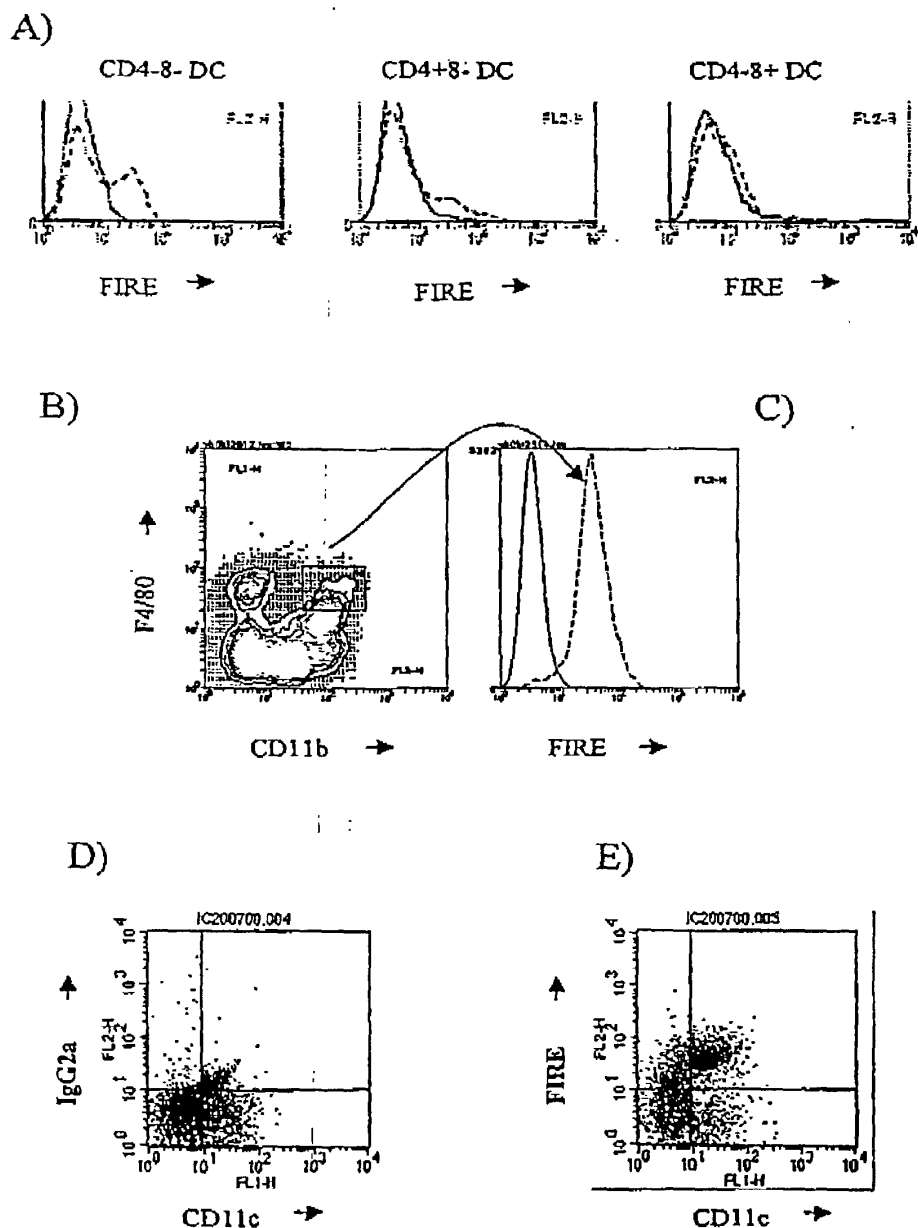


Figure 4

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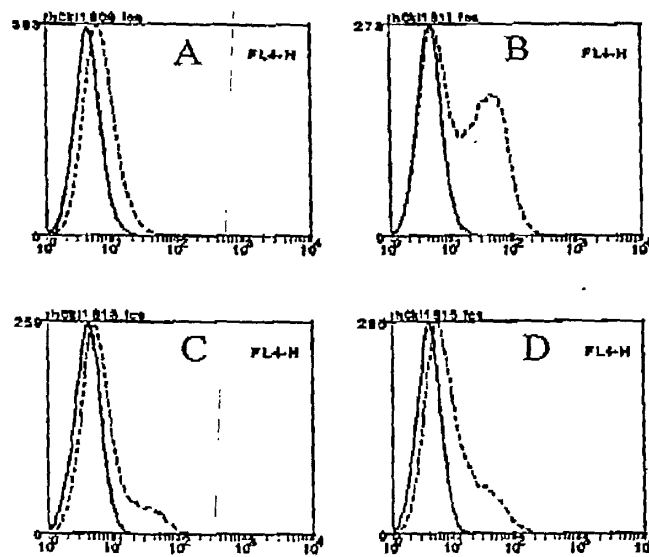


Figure 5

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Figure 6

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1671	F T I I N T L Q G V L L F V V H C L L N R O V R M E Y K K W	1710
	TTCCACATCAACACCTTCAGGAGATGTGCTCTTTGTGTACACTGTCTCTTANTGCCAGGTTGCAANTGGATATATAAAGTGG	
	F S G M R K G V E T E S T E M S R S T T Q T K T E E V G K S	1800
1711	TTTAGTGGAGTCCGGAAAGGGGTAGAAACTGAAAGCACTGAGATGCTCGCTCTACTACCCAAACCAAAACGGACAGCTGGGAGATCC	
	S E I F H K G G T A S S A E S T T K Q P Q P Q P Q V H L V S A A	1890
1801	TCRGAANAATCTTTCAAAAGGAGGCACTGCATCATCATCTGCAGAGGTCAACCCAGACGGTCAACAGGTTCACTCTGCTCTGCTGCT	
	W L K M N *	1980
1891	TGGCTAAAGATGNAATGACTGGCCAAAGTGCCTGGCATGACCCGGGAAGTTACGGCTCTCTTCCTGGTTGTCTACAGCGCCCTGTGCTCA	2070
1981	CACATAGATTGGACAATGCCACATATTTCTAGCTTCTCTGTGAAGAAGCTPAGGTCNTTCACTATTTTGGCTTTTATGTGTACATAGAAA	2160
2071	GAACAAGACATTTGGAGAAATCTTTAGATCCAGAGTGTGTGGCAGTGGCAATGAGGTCTGGAGAGATGGATTTTAAAGATGGC	2250
2161	GGCGGGAAGTGGATTTTCTTTGTGACGCTPACTGCCACCTGGCCAGAACTTCACTAACTGGCATCTGGRATTCAGCTCATAGTTCC	2340
2251	CTTTCTGCCTCTCTGCTGATTTTATGCTTCCCAAAGATTTTACATPACACTCCACATTCACATAATTCACAAATTTTCATATGAGATCA	2430
2341	GTATTAAGAGAGGTGTGCATTTTCCAAATACAAATATGCATATATCAGTGTGTGGAGATCTAGGAAGATPAGGAACACITTTTACACATGT	2520
2431	TGCTGGGACTCTAACTAGTTTCAACCATCGTGGAAATGATGTGGCATTTCTCAGGGATCTAGAGATACAGATPAGGAATACCTTTTACACAGCT	2610
2521	ATGCCATTAAGTGGATATATACCAAGGACTATTAATATGCTGCTATAAAGACACATGCACAGATATGTTTATGTGGCATTTATTCACA	2700
2611	ATAGCAAAAGACTTGGAAACCAACCAAGGATTCACCAATGNTAGATCGGATTAAGAAATGTGGCACATATACACCACGGATATCTATGCA	2790
2701	GCACATAAATGATGAGTTCATGTCTTTGTAGGGACATGGTGAATCCGGATTTCCCGGATCTACTACCGGGCTCCAGGAGTCTGCTCGC	
2791	CACCAATC 2798	

Figure 6 (continued)